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PIWI-interacting RNAs: new biomarkers for diagnosis and treatment of breast cancer

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Author Proof

Abstract

Cancer is one of the most important reasons of mortality in the world. However, there are several therapeutic platforms to treat patients who suffering from cancer common treatments such as surgery, chemotherapy and etc. The current therapeutic approaches are related to some limitations. Hence, more understanding about molecular mechanisms that involved in cancer particularly in breast cancer pathogenesis, could contribute to provide better therapeutic platforms. Recently, non-coding RNAs such as microRNAs have attracted researchers' attention in the field of cancer due to their functions in gene expression's regulation and functional interactions with other molecules. Interestingly, great advances in next-generation sequencing lead to considering other roles for another non-coding RNAs subgroup called PIWI-interacting RNAs (piRNAs) in addition to their functions in the germline. Novel studies investigated the role of piRNAs in several cancers including lung cancer, hepatocellular carcinoma, gastric cancer, multiple myeloma and colorectal cancer. Hopefully, based on new findings, piRNAs may be a potential biomarker which can be used as a tool to diagnose or treat breast cancer. Thus, this review aimed to discuss the role of piRNAs in breast cancer progression and metastasis as well as its molecular mechanisms.

Keywords: piRNA, Breast cancer, Epigenetic regulations

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Background

Breast disorders are very important disorders among women [1]. Among them, Breast cancer is the most common malignancy among women and it is the principle cause of women's death all over the world. In spite of great progress in the field of cancer, breast cancer is still a serious health problem among women which has complicated properties heterogeneously and shows a number of biological and clinical manifestations [2–4]. Breast cancer has been categorized into five groups based on expression patterns of three receptors: the estrogen receptor, progesterone receptor and human epidermal growth factor receptor. This categorization was a helpful way in order to predict the outcome and choose the best treatment option [5, 6]. Mutations in BRCA1 and BRCA2 are some examples of genomic instabilities which are the most prominent cause of breast cancer [7–9]. Several studies indicated that a variety of techniques could be used in the treatment of different cancers such as breast cancer (i.e., cell-, gene-, and nanotechnology-based therapies) [10–17]. Despite emerging new and effective therapeutic platforms in the treatment of breast cancer, new approaches are needed [18, 19]. In this regard, it seems that more understanding of cellular and molecular pathways involved in breast cancer pathogenesis could contribute to the development of new therapies [18].

In the past, scientists called 98% non-protein coding human genome as "junk" DNA. These DNAs produce RNAs which are not translated into proteins. This group is known as non-coding RNAs (non-encoding RNAs) which has two main subgroups: regulatory non-coding RNAs and housekeeping non-coding RNAs. The regulatory non-coding RNAs are also sorted into two subdivisions by their length: short chain non-coding RNAs and

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